

STIC-Biotech/ChemLib

125920

From: Kaufman, Claire  
Sent: Tuesday, June 29, 2004 12:26 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search 10/063,585

SEQUENCE SEARCH REQUEST

Examiner: Claire Kaufman AU: 1646 MAILBOX:Rem 4C70  
Room:Rem 4E85 Serial #:10/063,585 Date:6/29/04

Please search SEQ ID NO:75 and 76  
and fragment of SEQ ID NO:75 from nucleotide 121-957,  
and fragment of SEQ ID NO:76 from 1-139.  
in commercial databases.

Please put results on disk.

Thanks,  
Claire Kaufman, AU 1646  
Rem 4E85 (571) 272-0873

CBE

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

Art Unit: 1646

LOCUS BG741175 872 bp mRNA linear EST 15-MAY-2001  
DEFINITION 602631855F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4777165 5',  
mRNA sequence.

ACCESSION BG741175

VERSION BG741175.1 GI:14051828

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 872)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA

Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:<http://image.llnl.gov>

Plate: LLAM10630 row: n column: 14

High quality sequence start: 12

High quality sequence stop: 809.

FEATURES Location/Qualifiers

source

1..872

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4777165"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NCI\_CGAP\_Skn3"

/note="Organ: skin; Vector: pCMV-SPORT6; Site\_1: NotI;

Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.5kb. Library constructed by Life

Technologies. Note: this is a NCI\_CGAP Library."

ORIGIN

Query Match 44.8%; Score 781.4; DB 12; Length 872;

Best Local Similarity 95.1%; Pred. No. 8.4e-199;

Matches 828; Conservative 0; Mismatches 41; Indels 2; Gaps 2;

Qy 521 CAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTGGCCATATCTATTACCGTGTTC 580

Db 1 CAGACGTCAAGGCTAAATCCATCTTCTGGTATGTTTGGCCATATCTATTACCGTGTTC 60

Qy 581 TTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACACC 640

Db 61 TTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACACC 120

Qy 641 CAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTG 700

Db 121 CAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTG 180

Qy 701 AAAAAATCGTGATTAACCTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATC 760

Db 181 AAAAAATCGTGATTAACCTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATC 240

Group	Species	Position	Sequence	Position
5	Qy	761	AGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCA	820
	Db	241	AGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCA	300
10	Qy	821	GCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGC	880
	Db	301	GCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGC	360
15	Qy	881	ATTTGATGGAAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCTCACCAGC	940
	Db	361	ATTTGATGGAAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTTTACCAGC	420
20	Qy	941	AAGAGTCCCTCAGCAGAACAATACCCCGGATAAAAACAGTCATTGAATATGAATATGATG	1000
	Db	421	AAGAGTCCCTCAGCAGAACAATACCCCGGATAAAAACAGTCATTGAATATGAATATGATG	480
25	Qy	1001	TCAGAACCACTGACATTTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTTGCAGGAGGAGG	1060
	Db	481	TCAGAACCACTGACATTTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTTGCAGGAGGAGG	540
30	Qy	1061	TGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCAGAAA	1120
	Db	541	TGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCAGAAA	600
35	Qy	1121	CGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCACA	1180
	Db	601	CGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCACA	660
40	Qy	1181	CAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGATCCCC	1240
	Db	661	CAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGATCCCC	720
45	Qy	1241	AAACTGGC-AGGCTGTGTATTCTTCGCTGTCCAGCTTCGACCAGGATTAGAGGGC-TG	1298
	Db	721	AAACTGGCAAGGCTGTGTATTCTTCGCTGTCCAGCTTCGAACAGGATTAGAGGGCTTG	780
50	Qy	1299	CGAGCCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGA	1358
	Db	781	CGAGCCTTCTGAGGGGGATGGGCTCGGAAAAGGAAGGTCTCTATCTAGAACTCTATGAAGG	840
55	Qy	1359	GCCGGCTCCAGACAGGCCACCAGGAGAAAAT	1389
	Db	841	AGCCGGGTCAGACAGGGCACCAGGAGAAAAT	871

Art Unit: 1646

LOCUS BF056614 707 bp mRNA linear EST 16-OCT-2000  
DEFINITION 7k20c06.x1 NCI\_CGAP\_Ov18 Homo sapiens cDNA clone IMAGE:3475955 3'  
similar to TR:Q9UHF4 Q9UHF4 CLASS II CYTOKINE RECEPTOR ZCYTOR7. ; ,  
mRNA sequence.

5 ACCESSION BF056614  
VERSION BF056614.1 GI:10810598  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

10 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 707)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

15 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

20 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento

Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The

I.M.A.G.E. Consortium DNA Sequencing by: Washington University

Genome Sequencing Center

25 Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL, send email to:

[info@image.llnl.gov](mailto:info@image.llnl.gov)

Seq primer: -40UP from Gibco

High quality sequence stop: 459.

30 FEATURES Location/Qualifiers

source

1. 707

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3475955"

35 /tissue\_type="fibrotheoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NCI\_CGAP\_Ov18"

/note="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a

40 modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGGAGCGCGCGACATTTTTTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not

45 I and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

50 Query Match 36.9%; Score 642.4; DB 10; Length 707;

Best Local Similarity 95.9%; Pred. No. 2.1e-161;

Matches 681; Conservative 0; Mismatches 26; Indels 3; Gaps 2;

Qy 578 TTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAAC 637

55 Db 1 TTTT TTTT TTTT ATGT GTTGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAAC 60

Qy 638 ACCCAGCAAATTTGATTTTGATTATGGAATGAATTTGACAAAAGATTCTTTGTGCCTG 697

60 Db 61 ACCCAGCAAATTTGATTTTGATTATGGAATGAATTTGACAAAAGATTCTTTGTGCCTG 120

	Qy	698	CTGAAAAAATCGTGATTAACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTC	757
	Db	121	CTGAAAAAATCGTGATTAACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTC	180
5	Qy	758	ATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGC	817
	Db	181	ATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGC	240
10	Qy	818	CCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTT	877
	Db	241	CCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTT	300
	Qy	878	CGCATTTGATGGAAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCTCACCC	937
15	Db	301	CGCATTTGATGGAAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTTTCACCC	360
	Qy	938	AGCAAGAGTCCCTCAGCAGAACAATACCCCCGGATAAAACAGTCATTGAATATGAATATG	997
20	Db	361	AGCAAGAGTCCCTCAGCAGAACAATACCCCCGGATAAAACAGTCATTGAATATGAATATG	420
	Qy	998	ATGTCAGAACCACCTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGGAGG	1057
	Db	421	ATGTCAGAACCACCTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGGAGG	480
25	Qy	1058	AGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCCGC	1117
	Db	481	AGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCCGC	540
30	Qy	1118	AAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCCTGGCGCAGGAGC	1177
	Db	541	AAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCCTGGCGCAGGAGC	600
	Qy	1178	ACACAGACTCGGAGGAGGGGGCCGGAGAAGAGCCATCGACGACCCTGGTCGACTGGGATC	1237
35	Db	601	ACACAGAACTTCGGGAGGGGGCCGGAGAAGAGCCATCGACGACCCTGGTCGAC-CTGATC	659
	Qy	1238	CCCAAACCTGGCAGGCTGTGTATTCTTCGCTGTCCAGCTTCGACCAGGAT	1287
40	Db	660	CCCAAACCTGGCCAGCTGTG--ATCCCTTCGTGTCCAGCTTCACACAGGAT	707

Art Unit: 1646

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LOCUS       AA470014                563 bp    mRNA    linear    EST 08-AUG-1997
DEFINITION  zu10f04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731455
            5', mRNA sequence.
ACCESSION   AA470014
VERSION     AA470014.1  GI:2197323
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 563)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL    Unpublished (1997)
  COMMENT    Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 492.
FEATURES             Location/Qualifiers
     source          1..563
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:5928429"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:731455"
                     /sex="male"
                     /lab_host="DH10B"
                     /clone_lib="Soares_testis_NHT"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from Clontech
                     Laboratories, Inc., and primed with a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGCGCCGCAATTTTTTTTTTTTTTTTTT 3'].
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization to Cot5, and was
                     constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN
Query Match          30.9%;  Score 538.4;  DB 9;  Length 563;
Best Local Similarity 99.3%;  Pred. No. 1.9e-133;
Matches 561;  Conservative 0;  Mismatches 2;  Indels 2;  Gaps 2;

55 Qy      1080 ATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCGCAAACGTTACAGTACTCATACAC 1139
      |||
Db         1 ATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCGCAAACGTTACAGTACTCATACAC 60

Qy      1140 CCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGGCC 1199
      |||

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Art Unit: 1646

5 Db 61 CCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGGCC 120

Qy 1200 GGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGATCCCCAAACTGGCAGGCTGTGTAT 1259

5 Db 121 GGA-GAAGAGCCATCGACGACCCTGGTGNACTGGGATCCCCAAACTGGCAGGCTGTGTAT 179

Qy 1260 TCCTTCGCTGTCCAGCTTCGACCAGGATTAGAGGGCTGCGAGCCTTCTGAGGGGGATGG 1319

10 Db 180 TCCTTCGCTGTCCAGCTTCGACCAGGATTAGAGGGCTGCGAGCCTTCTGAGGGGGATGG 239

Qy 1320 GCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACC 1379

Db 240 GCTCGGAG-GGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACC 298

15 Qy 1380 AGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGTTATATGTGCAGAT 1439

Db 299 AGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGTTATATGTGCAGAT 358

20 Qy 1440 GGAAAACCTGATGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAACAAGTGAGTCAC 1499

Db 359 GGAAAACCTGATGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAACAAGTGAGTCAC 418

Qy 1500 CCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTTCAGTG 1559

25 Db 419 CCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTTCAGTG 478

Qy 1560 TCTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTGGTTCATG 1619

30 Db 479 TCTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTGGTTCATG 538

Qy 1620 CATGTAGGTCTCTTAACAATGATGG 1644

Db 539 CATGTAGGTCTCTTAACAATGATGG 563

35

OM protein - protein search, using sw model

Run on: July 1, 2004, 12:36:59 ; Search time 24.4028 Seconds  
(without alignments)  
1609.413 Million cell updates/sec

Title: US-10-063-585-76\_COPY\_1\_139  
Perfect score: 732  
Sequence: 1 MSYNGLHQRVFKELKLLTLC.....PSEKQCARTLKDQSSEFKAK 139

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	732	100.0	377	6	ABO27318	Abo27318 Human sec
2	732	100.0	377	6	ABO34204	Abo34204 Human sec
3	732	100.0	434	3	AAy99370	Aay99370 Human PRO
4	732	100.0	434	4	AAB66119	Aab66119 Protein o
5	732	100.0	442	4	AAB87563	Aab87563 Human PRO
6	732	100.0	442	5	ABG95888	Abg95888 Human sec
7	732	100.0	442	6	ABU90913	Abu90913 Novel hum
8	732	100.0	442	6	ABO33972	Abo33972 Human sec
9	732	100.0	442	6	ABU71989	Abu71989 Novel hum
10	732	100.0	442	6	ABU71543	Abu71543 Human sec



11	732	100.0	442	6	ABU90997	Abu90997	Human	PRO
12	732	100.0	442	6	ABU92513	Abu92513	Human	sec
13	732	100.0	442	6	ABU81183	Abu81183	Human	sec
14	732	100.0	442	6	ABO53297	Abo53297	Novel	hum
15	732	100.0	442	6	ABU98300	Abu98300	Novel	hum
16	732	100.0	442	6	ABU89305	Abu89305	Novel	hum
17	732	100.0	442	6	ABU82512	Abu82512	Novel	hum
18	732	100.0	442	6	ABU96476	Abu96476	Human	PRO
19	732	100.0	442	6	ABU72146	Abu72146	Human	PRO
20	732	100.0	442	6	ADB17133	Adb17133	Human	tra
21	732	100.0	442	6	ABQ44276	Abo44276	Human	sec
22	732	100.0	442	6	ABO33612	Abo33612	Novel	hum
23	732	100.0	442	6	ADA19938	Ada19938	Novel	hum
24	732	100.0	442	6	ADB17321	Adb17321	Human	tra
25	732	100.0	442	6	ADA20110	Ada20110	Novel	hum
26	732	100.0	442	6	ADA00407	Ada00407	Human	sec
27	732	100.0	442	7	ABO44465	Abo44465	Human	sec
28	732	100.0	442	7	ABO33489	Abo33489	Novel	hum
29	732	100.0	442	7	ADB85649	Adb85649	Novel	hum
30	732	100.0	442	7	ADB68328	Adb68328	Human	PRO
31	732	100.0	442	7	ADB68135	Adb68135	Human	PRO
32	732	100.0	442	7	ADB90952	Adb90952	Novel	hum
33	732	100.0	442	7	ADC07032	Adc07032	Human	PRO
34	732	100.0	442	7	ADC17973	Adc17973	Human	PRO
35	732	100.0	442	7	ADC17211	Adc17211	Mammalian	
36	732	100.0	442	7	ADC14909	Adc14909	Novel	hum
37	732	100.0	442	7	ADC52404	Adc52404	Novel	hum
38	732	100.0	442	7	ADD70619	Add70619	Human	sec
39	732	100.0	442	7	ADD39696	Add39696	Human	sec
40	732	100.0	442	7	ADD70142	Add70142	Human	sec
41	732	100.0	442	7	ADD36080	Add36080	Novel	hum
42	732	100.0	442	7	ADD38263	Add38263	Human	sec
43	732	100.0	442	7	ADD39219	Add39219	Human	sec
44	732	100.0	442	7	ADD38742	Add38742	Human	sec
45	732	100.0	442	7	ADD40173	Add40173	Human	sec



OM protein - protein search, using sw model

Run on: July 1, 2004, 12:42:09 ; Search time 20.0964 Seconds  
(without alignments)  
2153.046 Million cell updates/sec

Title: US-10-063-585-76\_COPY\_1\_139  
Perfect score: 732  
Sequence: 1 MSYNGLHQRVFKELKLLTLC.....PSEKQCARTLKDQSSEFKAK 139

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Score	Match	Length	DB	ID	Description
No.		%				

1	732	100.0	442	10	US-09-946-374-104	Sequence 104, App
2	732	100.0	442	12	US-10-063-745-76	Sequence 76, Appl
3	732	100.0	442	12	US-10-063-512-76	Sequence 76, Appl
4	732	100.0	442	12	US-10-063-513-76	Sequence 76, Appl
5	732	100.0	442	12	US-10-063-515-76	Sequence 76, Appl
6	732	100.0	442	12	US-10-063-549-76	Sequence 76, Appl
7	732	100.0	442	12	US-10-063-569-76	Sequence 76, Appl
8	732	100.0	442	12	US-10-063-551-76	Sequence 76, Appl
9	732	100.0	442	12	US-10-006-485A-104	Sequence 104, App
10	732	100.0	442	12	US-10-013-907A-104	Sequence 104, App
11	732	100.0	442	12	US-10-015-499A-104	Sequence 104, App
12	732	100.0	442	12	US-10-063-555-76	Sequence 76, Appl
13	732	100.0	442	12	US-10-063-563-76	Sequence 76, Appl
14	732	100.0	442	12	US-10-063-594-76	Sequence 76, Appl
15	732	100.0	442	12	US-10-063-553-76	Sequence 76, Appl
16	732	100.0	442	12	US-10-063-554-76	Sequence 76, Appl
17	732	100.0	442	12	US-10-013-910A-104	Sequence 104, App
18	732	100.0	442	12	US-10-226-254A-104	Sequence 104, App
19	732	100.0	442	12	US-10-015-395A-104	Sequence 104, App
20	732	100.0	442	13	US-10-006-867-76	Sequence 76, Appl
21	732	100.0	442	13	US-10-063-547-76	Sequence 76, Appl
22	732	100.0	442	14	US-10-063-616-76	Sequence 76, Appl
23	732	100.0	442	14	US-10-063-502-76	Sequence 76, Appl
24	732	100.0	442	14	US-10-006-856A-104	Sequence 104, App
25	732	100.0	442	14	US-10-063-518-76	Sequence 76, Appl
26	732	100.0	442	14	US-10-063-598-76	Sequence 76, Appl
27	732	100.0	442	14	US-10-227-693-76	Sequence 76, Appl
28	732	100.0	442	14	US-10-006-818A-104	Sequence 104, App
29	732	100.0	442	14	US-10-015-393A-104	Sequence 104, App
30	732	100.0	442	14	US-10-063-567-76	Sequence 76, Appl
31	732	100.0	442	14	US-10-015-869A-104	Sequence 104, App
32	732	100.0	442	14	US-10-063-538-76	Sequence 76, Appl
33	732	100.0	442	14	US-10-012-121A-104	Sequence 104, App
34	732	100.0	442	14	US-10-063-599-76	Sequence 76, Appl
35	732	100.0	442	14	US-10-006-116A-104	Sequence 104, App
36	732	100.0	442	14	US-10-006-117A-104	Sequence 104, App
37	732	100.0	442	14	US-10-017-527A-104	Sequence 104, App
38	732	100.0	442	14	US-10-013-913A-104	Sequence 104, App
39	732	100.0	442	14	US-10-063-595-76	Sequence 76, Appl
40	732	100.0	442	14	US-10-007-194A-104	Sequence 104, App
41	732	100.0	442	14	US-10-013-430A-104	Sequence 104, App
42	732	100.0	442	14	US-10-011-671A-104	Sequence 104, App
43	732	100.0	442	14	US-10-012-755A-104	Sequence 104, App
44	732	100.0	442	14	US-10-015-386A-104	Sequence 104, App
45	732	100.0	442	14	US-10-063-580-76	Sequence 76, Appl

OM protein - protein search, using sw model

Run on: July 1, 2004, 12:41:09 ; Search time 6.69879 Seconds  
 (without alignments)  
 1995.974 Million cell updates/sec

Title: US-10-063-585-76\_COPY\_1\_139  
 Perfect score: 732  
 Sequence: 1 MSYNGLHQRFVKELKLLTLC.....PSEKQCARTLKDQSSEFKAK 139

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_78:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	124	16.9	349	2	JC6311	interferon recepto
2	116	15.8	325	2	A47003	cytokine receptor
3	91.5	12.5	897	1	A39255	cytokine receptor
4	88	12.0	1014	2	T24412	hypothetical prote
5	87.5	12.0	896	1	A35782	cytokine receptor
6	84.5	11.5	1344	2	T14316	rig-1 protein - mo
7	82.5	11.3	1526	2	T19473	hypothetical prote
8	81.5	11.1	557	2	A32694	interferon alpha/b
9	80.5	11.0	590	2	A45283	interferon alpha/b
10	77.5	10.6	1198	2	G86849	hypothetical prote
11	77	10.5	250	2	JH0749	class II histocomp
12	76.5	10.5	1148	2	S72635	exo-poly-alpha-gal
13	75.5	10.3	295	2	AC2451	hypothetical prote
14	75.5	10.3	453	2	AB2122	hypothetical prote

15	75.5	10.3	1006	2	T41439	putitive sulfite r
16	74.5	10.2	884	2	T25205	hypothetical prote
17	74.5	10.2	984	1	A34076	protein-tyrosine k
18	74	10.1	509	2	JC5288	SHP substrate-1 pr
19	74	10.1	513	2	JC5289	SHP substrate-1 pr
20	74	10.1	590	2	A40437	glutamic acid-rich
21	73.5	10.0	166	2	S71209	ubiquitin-protein
22	73.5	10.0	167	2	S46656	ubiquitin-protein
23	73.5	10.0	805	2	S68441	leptin receptor, s
24	73.5	10.0	892	2	S68439	leptin receptor, s
25	73.5	10.0	894	2	S68437	leptin receptor, s
26	73.5	10.0	900	2	S68440	leptin receptor, s
27	73.5	10.0	1162	2	S68438	leptin receptor, s
28	73.5	10.0	1363	2	T43220	insulin-like growt
29	73.5	10.0	1825	2	C88400	protein H19M22.1 [
30	73.5	10.0	1825	2	T32828	hypothetical prote
31	73.5	10.0	2944	2	A54849	collagen alpha 1(V
32	73	10.0	530	2	S46322	phosphoprotein pho
33	73	10.0	1259	2	AE1055	probable exported
34	72.5	9.9	483	2	T16926	hypothetical prote
35	72	9.8	335	2	AF1125	phosphate transpor
36	72	9.8	1935	2	T39411	RNA helicase - fis
37	71.5	9.8	313	2	T28312	ORF MSV151 probabl
38	71	9.7	560	2	S27387	interferon alpha r
39	70.5	9.6	459	2	T11202	NADH2 dehydrogenas
40	70	9.6	591	2	S73790	hypothetical prote
41	70	9.6	778	2	T38347	aconitate hydratas
42	70	9.6	1122	2	I54237	protein-tyrosine k
43	70	9.6	1123	1	JN0712	protein-tyrosine k
44	70	9.6	1125	1	JH0771	protein-tyrosine k
45	70	9.6	1897	1	TDHULK	leukocyte antigen-

OM protein - protein search, using sw model

Run on: July 1, 2004, 12:37:34 ; Search time 4.78485 Seconds  
(without alignments)  
1512.638 Million cell updates/sec

Title: US-10-063-585-76\_COPY\_1\_139  
Perfect score: 732  
Sequence: 1 MSYNGLHQRVFKELKLLTLC.....PSEKQCARTLKDQSSEFKAK 139

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	123	16.8	349	1	I10S_MOUSE	Q61190 mus musculu
2	116	15.8	325	1	I10S_HUMAN	Q08334 homo sapien
3	91.5	12.5	897	1	CYRB_HUMAN	P32927 homo sapien
4	87.5	12.0	896	1	CYRB_MOUSE	P26955 mus musculu
5	82.5	11.3	534	1	EPA1_MOUSE	Q60750 mus musculu
6	81.5	11.1	557	1	INR1_HUMAN	P17181 homo sapien
7	80.5	11.0	590	1	INR1_MOUSE	P33896 mus musculu
8	75.5	10.3	1006	1	MT10_SCHPO	Q09878 schizosacch
9	74.5	10.2	884	1	SEC5_CAEEL	Q22706 caenorhabdi
10	74.5	10.2	976	1	EPA1_HUMAN	P21709 homo sapien
11	74	10.1	513	1	SHS1_MOUSE	P97797 m protein-t
12	74	10.1	1394	1	CNG4_BOVIN	Q28181 bos taurus
13	73.5	10.0	166	1	UBC7_ARATH	Q42540 arabidopsis
14	73.5	10.0	167	1	UBCE_ARATH	P42747 arabidopsis
15	73.5	10.0	1162	1	LEPR_MOUSE	P48356 mus musculu
16	73.5	10.0	1363	1	ILPR_BRALA	O02466 branchiosto
17	73.5	10.0	2944	1	CA17_HUMAN	Q02388 homo sapien
18	73	10.0	530	1	P2B_EMENI	P48457 emericella

19	73	10.0	796	1	TLR6_HUMAN	Q9y2c9	homo sapien
20	73	10.0	972	1	CTA1_BACCI	P94286	bacillus ci
21	72	9.8	520	1	VL2_HPV21	P50795	human papil
22	72	9.8	1195	1	KCH7_RAT	O54852	rattus norv
23	72	9.8	1693	1	SAS_DROME	Q04164	drosophila
24	72	9.8	1935	1	YBBA_SCHPO	O60072	schizosacch
25	71.5	9.8	468	1	LEU2_OCEIH	Q8en69	oceanobacil
26	71	9.7	353	1	A4GT_PANTR	Q9n291	p lactosylc
27	71	9.7	560	1	INR1_BOVIN	Q04790	bos taurus
28	71	9.7	1165	1	LEPR_PIG	O02671	sus scrofa
29	71	9.7	1195	1	KCH7_MOUSE	Q9er47	mus musculu
30	70	9.6	560	1	INR1_SHEEP	Q28589	ovis aries
31	70	9.6	591	1	YD72_MYCPN	P75409	mycoplasma
32	70	9.6	778	1	ACON_SCHPO	O13966	schizosacch
33	70	9.6	1122	1	TIE2_MOUSE	Q02858	mus musculu
34	70	9.6	1897	1	PTPF_HUMAN	P10586	homo sapien
35	69.5	9.5	985	1	EP4B_XENLA	Q91694	xenopus lae
36	69.5	9.5	1110	1	VGLM_INSV	Q01260	impatiens n
37	69	9.4	475	1	PAAH_ECOLI	P76083	escherichia
38	69	9.4	574	1	TYRO_PODAN	Q92396	podospora a
39	68.5	9.4	143	1	YOAW_BACSU	O34541	bacillus su
40	68.5	9.4	878	1	PMPI_CHLTR	O84882	chlamydia t
41	68.5	9.4	1010	1	CONT_CHICK	P14781	gallus gall
42	68.5	9.4	1300	1	POL2_MOUSE	P11369	mus musculu
43	68	9.3	327	1	A4GT_GORGO	Q9n290	g lactosylc
44	68	9.3	353	1	A4GT_HUMAN	Q9npc4	h lactosylc
45	68	9.3	413	1	HEM1_COXBU	P47846	coxiella bu



5 OM nucleic - nucleic search, using sw model

Run on: July 1, 2004, 20:14:58 ; Search time 4797.3 Seconds  
(without alignments)  
15747.786 Million cell updates/sec

10 Title: US-10-063-585-75  
Perfect score: 1743  
Sequence: 1 tgcgcgtgccgcgcgtgctg.....gaatttattcaggtgggtgt 1743

15 Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

20 Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

25 Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*

30 1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

35 6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

40 11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vi:\*

15: em\_ba:\*

45 16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

50 21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

55 26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vi:\*

30: em\_htg\_hum:\*

60 31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htg\_mus:\*

34: em\_htg\_pln:\*

35: em\_htg\_rod:\*  
 36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Result		%	Query																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
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Run on: July 1, 2004, 18:10:20 ; Search time 526.278 Seconds  
 (without alignments)  
 14069.770 Million cell updates/sec

5 Title: US-10-063-585-75  
 Perfect score: 1743  
 Sequence: 1 tgccgctgccgcccgtgctg.....gaatttattcaggtgggtgt 1743

10 Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

15 Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

20 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
 25 1: geneseqn1980s:\*  
 2: geneseqn1990s:\*  
 3: geneseqn2000s:\*  
 4: geneseqn2001as:\*  
 5: geneseqn2001bs:\*  
 30 6: geneseqn2002s:\*  
 7: geneseqn2003as:\*  
 8: geneseqn2003bs:\*  
 9: geneseqn2003cs:\*  
 35 10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### 40 SUMMARIES

	Result No.	Score	% Query		DB	ID	Description
			Match	Length			
45	1	1743	100.0	1743	3	AAA37052	Aaa37052 Human PRO
	2	1743	100.0	1743	4	AAF54274	Aaf54274 DNA encod
	3	1743	100.0	1743	4	AAF92095	Aaf92095 Human PRO
	4	1743	100.0	1743	6	ABS74415	Abs74415 Human cDN
	5	1743	100.0	1743	7	ACA91201	Aca91201 Novel hum
50	6	1743	100.0	1743	7	ACD81578	Acd81578 Human cDN
	7	1743	100.0	1743	7	ACA60400	Aca60400 Novel hum
	8	1743	100.0	1743	7	ACA58847	Aca58847 cDNA enco
	9	1743	100.0	1743	7	ACA64023	Aca64023 cDNA enco
	10	1743	100.0	1743	7	ACA91287	Aca91287 cDNA enco
55	11	1743	100.0	1743	7	ACD45186	Acd45186 Human sec
	12	1743	100.0	1743	7	ACA93734	Aca93734 Human cDN
	13	1743	100.0	1743	7	ACA67308	Aca67308 cDNA enco
	14	1743	100.0	1743	7	ACH66281	Ach66281 Novel hum
	15	1743	100.0	1743	7	ACD02335	Acd02335 Novel hum
60	16	1743	100.0	1743	7	ACA89326	Aca89326 Novel hum
	17	1743	100.0	1743	7	ACA68963	Aca68963 Novel hum
	18	1743	100.0	1743	7	ACA98485	Aca98485 Human PRO
	19	1743	100.0	1743	8	ACA63410	Aca63410 cDNA enco

	20	1743	100.0	1743	8	ADB17132	Adb17132	Human	cDN
	21	1743	100.0	1743	8	ACH03613	Ach03613	Human	sec
	22	1743	100.0	1743	8	ACD68311	Acd68311	Novel	hum
	23	1743	100.0	1743	8	ADA19937	Ada19937	Novel	hum
5	24	1743	100.0	1743	8	ADB17320	Adb17320	Human	cDN
	25	1743	100.0	1743	8	ADA20109	Ada20109	Novel	hum
	26	1743	100.0	1743	8	ACD82127	Acd82127	Human	sec
	27	1743	100.0	1743	8	ADA00406	Ada00406	Human	sec
	28	1743	100.0	1743	8	ACH04413	Ach04413	Human	cDN
10	29	1743	100.0	1743	8	ACD67957	Acd67957	Novel	hum
	30	1743	100.0	1743	8	ADB85648	Adb85648	Novel	hum
	31	1743	100.0	1743	9	ADB68327	Adb68327	Human	PRO
	32	1743	100.0	1743	9	ADB68134	Adb68134	Human	PRO
	33	1743	100.0	1743	9	ADB90951	Adb90951	Novel	hum
15	34	1743	100.0	1743	9	ADC07031	Adc07031	Human	PRO
	35	1743	100.0	1743	9	ADC17972	Adc17972	Human	PRO
	36	1743	100.0	1743	9	ADC17210	Adc17210	cDNA	sequ
	37	1743	100.0	1743	9	ADC14908	Adc14908	Novel	hum
	38	1743	100.0	1743	9	ADC52403	Adc52403	Novel	hum
20	39	1743	100.0	1743	9	ADD70618	Add70618	Human	cDN
	40	1743	100.0	1743	9	ADD39695	Add39695	Human	cDN
	41	1743	100.0	1743	9	ADD70141	Add70141	Human	cDN
	42	1743	100.0	1743	9	ADD36079	Add36079	Novel	hum
	43	1743	100.0	1743	9	ADD38262	Add38262	Human	cDN
25	44	1743	100.0	1743	9	ADD39218	Add39218	Human	cDN
	45	1743	100.0	1743	9	ADD38741	Add38741	Human	cDN

30 Run on: July 1, 2004, 21:38:32 ; Search time 597.214 Seconds  
(without alignments)  
14079.701 Million cell updates/sec

35 Title: US-10-063-585-75  
Perfect score: 1743  
Sequence: 1 tgccgctgccgcccgcgtgctg.....gaattttattcaggtgggtgt 1743

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

40 Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

45 Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
50 Listing first 45 summaries

Database : Published\_Applications\_NA:\*

	1:	/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
	2:	/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
55	3:	/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
	4:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
	5:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
	6:	/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
	7:	/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
60	8:	/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
	9:	/cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
	10:	/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
	11:	/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2:\*  
 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
 16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
 17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
 18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
 19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
20	1	1743	100.0	1743	10	US-09-946-374-103
	2	1743	100.0	1743	12	US-10-015-395A-103
	3	1743	100.0	1743	13	US-10-063-745-75
	4	1743	100.0	1743	13	US-10-063-512-75
	5	1743	100.0	1743	13	US-10-063-513-75
25	6	1743	100.0	1743	13	US-10-063-515-75
	7	1743	100.0	1743	13	US-10-063-549-75
	8	1743	100.0	1743	13	US-10-063-569-75
	9	1743	100.0	1743	13	US-10-063-551-75
	10	1743	100.0	1743	13	US-10-006-485A-103
30	11	1743	100.0	1743	13	US-10-013-907A-103
	12	1743	100.0	1743	13	US-10-015-499A-103
	13	1743	100.0	1743	13	US-10-063-555-75
	14	1743	100.0	1743	13	US-10-063-563-75
	15	1743	100.0	1743	13	US-10-063-594-75
35	16	1743	100.0	1743	13	US-10-063-553-75
	17	1743	100.0	1743	13	US-10-063-554-75
	18	1743	100.0	1743	13	US-10-226-254A-103
	19	1743	100.0	1743	14	US-10-006-867-75
	20	1743	100.0	1743	14	US-10-063-547-75
40	21	1743	100.0	1743	15	US-10-063-616-75
	22	1743	100.0	1743	15	US-10-063-502-75
	23	1743	100.0	1743	15	US-10-006-856A-103
	24	1743	100.0	1743	15	US-10-063-518-75
	25	1743	100.0	1743	15	US-10-063-598-75
45	26	1743	100.0	1743	15	US-10-227-693-75
	27	1743	100.0	1743	15	US-10-006-818A-103
	28	1743	100.0	1743	15	US-10-015-393A-103
	29	1743	100.0	1743	15	US-10-063-567-75
	30	1743	100.0	1743	15	US-10-015-869A-103
50	31	1743	100.0	1743	15	US-10-012-121A-103
	32	1743	100.0	1743	15	US-10-063-599-75
	33	1743	100.0	1743	15	US-10-006-116A-103
	34	1743	100.0	1743	15	US-10-006-117A-103
	35	1743	100.0	1743	15	US-10-017-527A-103
55	36	1743	100.0	1743	15	US-10-013-913A-103
	37	1743	100.0	1743	15	US-10-063-595-75
	38	1743	100.0	1743	15	US-10-007-194A-103
	39	1743	100.0	1743	15	US-10-013-430A-103
	40	1743	100.0	1743	15	US-10-011-671A-103
60	41	1743	100.0	1743	15	US-10-012-755A-103
	42	1743	100.0	1743	15	US-10-015-386A-103
	43	1743	100.0	1743	15	US-10-063-580-75
	44	1743	100.0	1743	15	US-10-011-692A-103
	45	1743	100.0	1743	15	US-10-063-557-75

Run on: July 1, 2004, 21:35:43 ; Search time 3396.15 Seconds  
(without alignments)  
15326.124 Million cell updates/sec

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Title: US-10-063-585-75  
Perfect score: 1743  
Sequence: 1 tgccgctgccgcccgtgctg.....gaatttattcaggtgggtgt 1743

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

15

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database : EST:\*

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1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

60

Result	Query	
No.	Score	Match Length DB ID Description

	1	835.4	47.9	1150	29	AY402567	AY402567 Homo sapi
	2	795.2	45.6	922	14	CA454197	CA454197 AGENCOURT
	3	781.4	44.8	872	12	BG741175	BG741175 602631855
	4	675.4	38.7	2089	11	AK054215	AK054215 Mus muscu
5	5	642.4	36.9	707	10	BF056614	BF056614 7k20c06.x
	6	620.4	35.6	650	12	BM929674	BM929674 UI-E-EJ1-
	c 7	619.8	35.6	651	12	BM683620	BM683620 UI-E-EJ1-
	c 8	604.2	34.7	626	14	CK299400	CK299400 UI-E-EJ1-
	9	594.4	34.1	666	13	BQ187458	BQ187458 UI-E-EJ1-
10	c 10	573	32.9	590	13	BQ185521	BQ185521 UI-E-EJ1-
	11	557.6	32.0	1148	29	AY402568	AY402568 Pan trogl
	12	538.4	30.9	563	9	AA470014	AA470014 zu10f04.r
	13	536	30.8	536	14	CB128408	CB128408 K-EST0177
	14	510	29.3	510	10	BE218809	BE218809 hv45a06.x
15	c 15	505	29.0	507	10	BE219979	BE219979 hv65d06.x
	c 16	497	28.5	500	9	AA412292	AA412292 zu10g06.s
	17	488	28.0	497	10	BF110234	BF110234 7n51c05.x
	c 18	481	27.6	481	9	AA632915	AA632915 nm14g01.s
	c 19	468	26.9	469	9	AI147693	AI147693 qb43a10.x
20	c 20	461	26.4	469	9	AI347038	AI347038 qp54h11.x
	c 21	460	26.4	474	13	BX109816	BX109816 BX109816
	c 22	447	25.6	458	9	AI308941	AI308941 qc65d06.x
	23	440	25.2	449	10	BF445367	BF445367 7q81e02.x
25	c 24	428	24.6	430	9	AA836857	AA836857 of35a05.s
	c 25	427.2	24.5	447	9	AA135185	AA135185 zo27a05.s
	c 26	420	24.1	430	9	AA583432	AA583432 mn38a08.s
	c 27	418	24.0	442	9	AA018749	AA018749 ze51a05.r
	28	415.6	23.8	423	9	AI701862	AI701862 we30f09.x
	c 29	384.4	22.1	474	9	AA528216	AA528216 nj16h06.s
30	c 30	374.4	21.5	436	9	AA516435	AA516435 ne58a10.s
	c 31	373.4	21.4	437	10	BE645384	BE645384 7e80g02.x
	32	372	21.3	396	9	AA134881	AA134881 zm80b07.r
	33	371.4	21.3	472	9	AA018585	AA018585 ze51a05.s
	c 34	363.4	20.8	365	10	BE145495	BE145495 IL5-HT019
35	c 35	358	20.5	366	9	AA916348	AA916348 oh80e05.s
	36	352	20.2	608	14	N79409	N79409 yz74d05.r1
	37	346.4	19.9	417	9	AA494556	AA494556 ne38h08.s
	38	342.2	19.6	571	10	BE683868	BE683868 183856 MA
	39	336.4	19.3	399	14	R14678	R14678 yf92b08.r1
40	c 40	332	19.0	332	9	AA514541	AA514541 nf58b11.s
	41	327.6	18.8	1120	29	AY402569	AY402569 Mus muscu
	c 42	313	18.0	313	9	AI350971	AI350971 qq24h11.x
	c 43	312.8	17.9	326	14	N62509	N62509 yz74d05.s1
	44	304.4	17.5	691	10	AW241977	AW241977 xn77e09.x
45	45	297.4	17.1	451	14	H17201	H17201 ym37h05.r1

Run on: July 1, 2004, 12:36:59 ; Search time 77.5973 Seconds  
(without alignments)  
1609.413 Million cell updates/sec

Title: US-10-063-585-76  
Perfect score: 2324  
Sequence: 1 MSYNGLHQRVFKELKLLTLC.....NETYLMQFMEEWGLYVQMEN 442

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	2324	100.0	442	4	AAB87563	Aab87563 Human PRO
	2	2324	100.0	442	5	ABG95888	Abg95888 Human sec
	3	2324	100.0	442	6	ABU90913	Abu90913 Novel hum
	4	2324	100.0	442	6	ABO33972	Abo33972 Human sec
	5	2324	100.0	442	6	ABU71989	Abu71989 Novel hum
	6	2324	100.0	442	6	ABU71543	Abu71543 Human sec
	7	2324	100.0	442	6	ABU90997	Abu90997 Human PRO
	8	2324	100.0	442	6	ABU92513	Abu92513 Human sec
	9	2324	100.0	442	6	ABU81183	Abu81183 Human sec
	10	2324	100.0	442	6	ABO53297	Abo53297 Novel hum
	11	2324	100.0	442	6	ABU98300	Abu98300 Novel hum
	12	2324	100.0	442	6	ABU89305	Abu89305 Novel hum
	13	2324	100.0	442	6	ABU82512	Abu82512 Novel hum
	14	2324	100.0	442	6	ABU96476	Abu96476 Human PRO
	15	2324	100.0	442	6	ABU72146	Abu72146 Human PRO
	16	2324	100.0	442	6	ADB17133	Adb17133 Human tra
	17	2324	100.0	442	6	ABO44276	Abo44276 Human sec
	18	2324	100.0	442	6	ABO33612	Abo33612 Novel hum
	19	2324	100.0	442	6	ADA19938	Ada19938 Novel hum
	20	2324	100.0	442	6	ADB17321	Adb17321 Human tra
	21	2324	100.0	442	6	ADA20110	Ada20110 Novel hum
	22	2324	100.0	442	6	ADA00407	Ada00407 Human sec
	23	2324	100.0	442	7	ABO44465	Abo44465 Human sec
	24	2324	100.0	442	7	ABO33489	Abo33489 Novel hum
	25	2324	100.0	442	7	ADB85649	Adb85649 Novel hum
	26	2324	100.0	442	7	ADB68328	Adb68328 Human PRO
	27	2324	100.0	442	7	ADB68135	Adb68135 Human PRO
	28	2324	100.0	442	7	ADB90952	Adb90952 Novel hum
	29	2324	100.0	442	7	ADC07032	Adc07032 Human PRO
	30	2324	100.0	442	7	ADC17973	Adc17973 Human PRO
	31	2324	100.0	442	7	ADC17211	Adc17211 Mammalian
	32	2324	100.0	442	7	ADC14909	Adc14909 Novel hum
	33	2324	100.0	442	7	ADC52404	Adc52404 Novel hum
	34	2324	100.0	442	7	ADD70619	Add70619 Human sec
	35	2324	100.0	442	7	ADD39696	Add39696 Human sec
	36	2324	100.0	442	7	ADD70142	Add70142 Human sec
	37	2324	100.0	442	7	ADD36080	Add36080 Novel hum
	38	2324	100.0	442	7	ADD38263	Add38263 Human sec



	39	2324	100.0	442	7	ADD39219	Add39219 Human sec
	40	2324	100.0	442	7	ADD38742	Add38742 Human sec
	41	2324	100.0	442	7	ADD40173	Add40173 Human sec
	42	2324	100.0	442	7	ADE50394	Ade50394 Human sec
5	43	2324	100.0	442	7	ADE20006	Ade20006 Human sec
	44	2324	100.0	442	7	ADE49917	Ade49917 Human sec
	45	2324	100.0	442	7	ADE21475	Ade21475 Human sec

# 10 OM protein - protein search, using sw model

Run on: July 1, 2004, 12:42:09 ; Search time 63.9036 Seconds  
(without alignments)  
2153.046 Million cell updates/sec

15 Title: US-10-063-585-76  
Perfect score: 2324  
Sequence: 1 MSYNGLHQRVFKELKLLTLC.....NETYLMQFMEEWGLYVQMEN 442

20 Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

25 Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

30 Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

35	1:	/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
	2:	/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
	3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
	4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
	5:	/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
40	6:	/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
	7:	/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
	8:	/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
	9:	/cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
	10:	/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
45	11:	/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
	12:	/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
	13:	/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
	14:	/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
	15:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
50	16:	/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
	17:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
	18:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

55 Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	2324	100.0	442	10	US-09-946-374-104	Sequence 104, App	

	2	2324	100.0	442	12	US-10-063-745-76	Sequence 76, Appl
	3	2324	100.0	442	12	US-10-063-512-76	Sequence 76, Appl
	4	2324	100.0	442	12	US-10-063-513-76	Sequence 76, Appl
	5	2324	100.0	442	12	US-10-063-515-76	Sequence 76, Appl
5	6	2324	100.0	442	12	US-10-063-549-76	Sequence 76, Appl
	7	2324	100.0	442	12	US-10-063-569-76	Sequence 76, Appl
	8	2324	100.0	442	12	US-10-063-551-76	Sequence 76, Appl
	9	2324	100.0	442	12	US-10-006-485A-104	Sequence 104, App
	10	2324	100.0	442	12	US-10-013-907A-104	Sequence 104, App
10	11	2324	100.0	442	12	US-10-015-499A-104	Sequence 104, App
	12	2324	100.0	442	12	US-10-063-555-76	Sequence 76, Appl
	13	2324	100.0	442	12	US-10-063-563-76	Sequence 76, Appl
	14	2324	100.0	442	12	US-10-063-594-76	Sequence 76, Appl
	15	2324	100.0	442	12	US-10-063-553-76	Sequence 76, Appl
15	16	2324	100.0	442	12	US-10-063-554-76	Sequence 76, Appl
	17	2324	100.0	442	12	US-10-013-910A-104	Sequence 104, App
	18	2324	100.0	442	12	US-10-226-254A-104	Sequence 104, App
	19	2324	100.0	442	12	US-10-015-395A-104	Sequence 104, App
	20	2324	100.0	442	13	US-10-006-867-76	Sequence 76, Appl
20	21	2324	100.0	442	13	US-10-063-547-76	Sequence 76, Appl
	22	2324	100.0	442	14	US-10-063-616-76	Sequence 76, Appl
	23	2324	100.0	442	14	US-10-063-502-76	Sequence 76, Appl
	24	2324	100.0	442	14	US-10-006-856A-104	Sequence 104, App
	25	2324	100.0	442	14	US-10-063-518-76	Sequence 76, Appl
25	26	2324	100.0	442	14	US-10-063-598-76	Sequence 76, Appl
	27	2324	100.0	442	14	US-10-227-693-76	Sequence 76, Appl
	28	2324	100.0	442	14	US-10-006-818A-104	Sequence 104, App
	29	2324	100.0	442	14	US-10-015-393A-104	Sequence 104, App
	30	2324	100.0	442	14	US-10-063-567-76	Sequence 76, Appl
30	31	2324	100.0	442	14	US-10-015-869A-104	Sequence 104, App
	32	2324	100.0	442	14	US-10-063-538-76	Sequence 76, Appl
	33	2324	100.0	442	14	US-10-012-121A-104	Sequence 104, App
	34	2324	100.0	442	14	US-10-063-599-76	Sequence 76, Appl
	35	2324	100.0	442	14	US-10-006-116A-104	Sequence 104, App
35	36	2324	100.0	442	14	US-10-006-117A-104	Sequence 104, App
	37	2324	100.0	442	14	US-10-017-527A-104	Sequence 104, App
	38	2324	100.0	442	14	US-10-013-913A-104	Sequence 104, App
	39	2324	100.0	442	14	US-10-063-595-76	Sequence 76, Appl
	40	2324	100.0	442	14	US-10-007-194A-104	Sequence 104, App
40	41	2324	100.0	442	14	US-10-013-430A-104	Sequence 104, App
	42	2324	100.0	442	14	US-10-011-671A-104	Sequence 104, App
	43	2324	100.0	442	14	US-10-012-755A-104	Sequence 104, App
	44	2324	100.0	442	14	US-10-015-386A-104	Sequence 104, App
45	45	2324	100.0	442	14	US-10-063-580-76	Sequence 76, Appl

OM protein - protein search, using sw model

Run on: July 1, 2004, 12:41:09 ; Search time 21.3012 Seconds  
(without alignments)  
1995.974 Million cell updates/sec

Title: US-10-063-585-76  
Perfect score: 2324  
Sequence: 1 MSYNGLHQRVFKELKLLTLC.....NETYLMQFMEEWGLYVQMEN 442

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	%		DB	ID	Description
		Match	Length			
1	162	7.0	349	2	JC6311	interferon recepto
2	137	5.9	325	2	A47003	cytokine receptor
3	124.5	5.4	575	2	A49667	interleukin-10 rec
4	122.5	5.3	3924	2	S37431	ankyrin 2, neurona
5	117.5	5.1	1912	2	A56178	protein-tyrosine-p
6	116	5.0	354	2	T24873	hypothetical prote
7	115.5	5.0	1222	2	C88504	protein B0361.3 [i
8	115	4.9	2957	2	T33152	hypothetical prote
9	114	4.9	776	2	A46583	neuroendocrine-spe
10	113.5	4.9	896	1	A35782	cytokine receptor
11	113	4.9	672	2	AH2992	hypothetical prote
12	113	4.9	672	2	B98291	hypothetical prote
13	112	4.8	1089	2	T14576	nosA protein - sli
14	111	4.8	501	2	C71948	hypothetical prote
15	111	4.8	1805	2	A34736	nestin - rat
16	110	4.7	5376	2	T42215	zonadhesin - mouse
17	109	4.7	3507	2	T34513	hypothetical prote
18	108	4.6	848	2	S48273	probable transcrip
19	108	4.6	1039	2	T09883	hypothetical prote
20	107	4.6	862	2	S43922	versican - pig-tai
21	107	4.6	4910	2	S64942	probable membrane
22	106.5	4.6	897	1	A39255	cytokine receptor
23	106.5	4.6	1317	2	T03748	apoptosis associat
24	105	4.5	536	2	T27668	hypothetical prote
25	105	4.5	540	2	T44967	gas-vesicle protei
26	105	4.5	590	2	A40437	glutamic acid-rich
27	104.5	4.5	2477	2	S14428	fibronectin precur
28	104	4.5	505	2	B64560	poly E-rich protei
29	104	4.5	918	2	A44257	interleukin-6 sign
30	103.5	4.5	918	2	A36337	membrane glycoprot
31	103.5	4.5	5762	2	A41819	proline-rich pepti
32	103	4.4	1162	2	S68438	leptin receptor, s
33	102.5	4.4	477	2	A34368	interferon gamma r
34	102.5	4.4	896	2	I56563	interleukin-3 rece
35	102	4.4	989	2	T47503	hypothetical prote
36	102	4.4	1894	2	C54689	protein-tyrosine-p
37	101.5	4.4	500	2	F88921	protein F56E10.3 [
38	101.5	4.4	638	2	S54418	fibronectin-bindin
39	101.5	4.4	1079	2	A86220	protein F22013.29
40	101.5	4.4	1113	2	T00736	hypothetical prote
41	101.5	4.4	2464	1	QRMSPI	microtubule-associ
42	100.5	4.3	740	2	T03847	Fas-binding protei

43	100.5	4.3	768	2	H54024	protein kinase (EC
44	100.5	4.3	777	2	B54024	protein kinase (EC
45	100.5	4.3	777	2	F54024	protein kinase (EC

5

OM protein - protein search, using sw model

Run on: July 1, 2004, 12:37:34 ; Search time 15.2151 Seconds  
(without alignments)  
1512.638 Million cell updates/sec

10

Title: US-10-063-585-76  
Perfect score: 2324  
Sequence: 1 MSYNGLHQVRVFKELKLLTLC.....NETYLMQFMEEWGLYVQMEN 442

15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

20

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

30

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

35

# SUMMARIES

Result No.	Score	% Match	Query Length	IDB	ID	Description
40	1	161	6.9	349	1	I10S_MOUSE Q61190 mus musculu
	2	137	5.9	325	1	I10S_HUMAN Q08334 homo sapien
	3	124.5	5.4	575	1	I10R_MOUSE Q61727 mus musculu
	4	122.5	5.3	3924	1	ANK2_HUMAN Q01484 homo sapien
45	5	121	5.2	530	1	INR2_BOVIN Q95141 bos taurus
	6	117.5	5.1	1912	1	PTPD_HUMAN P23468 homo sapien
	7	115	4.9	536	1	INR2_SHEEP Q95207 ovis aries
	8	114	4.9	776	1	RTN1_HUMAN Q16799 homo sapien
	9	113.5	4.9	896	1	CYRB_MOUSE P26955 mus musculu
50	10	112	4.8	1221	1	YMP3_CAEEL Q10947 caenorhabdi
	11	111	4.8	1805	1	NEST_RAT P21263 rattus norv
	12	110.5	4.8	795	1	CDL1_HUMAN P21127 homo sapien
	13	110.5	4.8	950	1	STL2_MOUSE Q99n50 mus musculu
	14	110	4.7	5376	1	ZAN_MOUSE O88799 mus musculu
55	15	108.5	4.7	2477	1	FINC_MOUSE P11276 mus musculu
	16	108	4.6	848	1	YBV8_YEAST P38266 saccharomyc
	17	107	4.6	862	1	PGCV_MACNE Q28858 macaca neme
	18	107	4.6	1505	1	CUT2_HUMAN O14529 homo sapien
	19	107	4.6	4910	1	MDN1_YEAST Q12019 saccharomyc
60	20	105.5	4.5	897	1	CYRB_HUMAN P32927 homo sapien
	21	105.5	4.5	931	1	SFB1_RAT O88453 rattus norv
	22	105	4.5	1394	1	CNG4_BOVIN Q28181 bos taurus
	23	104.5	4.5	2477	1	FINC_RAT P04937 rattus norv

	24	104	4.5	380	1	LE22_PYRFU	Q8u0c0	pyrococcus
	25	104	4.5	521	1	RUN2_HUMAN	Q13950	h runt-rela
	26	104	4.5	780	1	CDL2_HUMAN	Q9uq88	homo sapien
	27	104	4.5	918	1	IL6B_RAT	P40190	rattus norv
5	28	103.5	4.5	918	1	IL6B_HUMAN	P40189	homo sapien
	29	103.5	4.5	988	1	E4L2_MOUSE	O70318	mus musculu
	30	103	4.4	941	1	VDP_MOUSE	Q9z1z0	mus musculu
	31	103	4.4	1162	1	LEPR_MOUSE	P48356	mus musculu
	32	103	4.4	5038	1	PCLO_MOUSE	Q9qyx7	mus musculu
10	33	102.5	4.4	440	1	BRA2_BRAFL	P80492	branchiosto
	34	102.5	4.4	477	1	INGR_MOUSE	P15261	mus musculu
	35	102.5	4.4	870	1	Y563_HUMAN	O60309	homo sapien
	36	102.5	4.4	1123	1	RBM6_HUMAN	P78332	homo sapien
	37	102	4.4	555	1	ZF38_MOUSE	Q07231	mus musculu
15	38	101.5	4.4	2464	1	MAPB_MOUSE	P14873	mus musculu
	39	101	4.3	895	1	STL2_HUMAN	Q9hch5	homo sapien
	40	101	4.3	1948	1	PTNS_HUMAN	Q13332	homo sapien
	41	100.5	4.3	740	1	DAXX_HUMAN	Q9uer7	homo sapien
	42	100	4.3	896	1	EP15_HUMAN	P42566	homo sapien
20	43	100	4.3	915	1	SFB1_HUMAN	Q15424	homo sapien
	44	100	4.3	1010	1	Y226_HUMAN	Q92622	homo sapien
	45	100	4.3	5085	1	PCLO_RAT	Q9jks6	rattus norv

25 Run on: July 1, 2004, 12:40:39 ; Search time 54.0138 Seconds  
(without alignments)  
2581.917 Million cell updates/sec

Title: US-10-063-585-76  
Perfect score: 2324  
30 Sequence: 1 MSYNGLHQRVFKELKLLTLC.....NETYLMQFMEEWGLYVQMEN 442

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

35 Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

40 Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

45 Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
50 3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
55 9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
60 13: sp\_vertibrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5

# SUMMARIES

Result	% Query					ID	Description
	No.	Score	Match	Length	DB		
10	1	2206	94.9	553	4	Q96SH8	Q96sh8 homo sapien
	2	2203	94.8	553	4	Q9UHF4	Q9uhf4 homo sapien
	3	1239	53.3	546	11	Q8BW64	Q8bw64 mus musculu
	4	303.5	13.1	209	4	Q96SH7	Q96sh7 homo sapien
15	5	263.5	11.3	568	13	Q800F7	Q800f7 tetraodon n
	6	262.5	11.3	568	13	Q800G1	Q800g1 tetraodon n
	7	161	6.9	351	11	Q8VHM7	Q8vhm7 mus musculu
	8	138	5.9	341	13	Q9YGC8	Q9ygc8 gallus gall
20	9	137	5.9	325	4	Q9BUU4	Q9buu4 homo sapien
	10	131	5.6	508	13	Q9PVK0	Q9pvk0 gallus gall
	11	130	5.6	16223	5	Q8IR22	Q8ir22 drosophila
	12	128.5	5.5	1487	10	Q9FH23	Q9fh23 arabidopsis
25	13	126.5	5.4	896	13	Q8JFR9	Q8jfr9 brachydanio
	14	125	5.4	1863	4	Q7Z3L5	Q7z3l5 homo sapien
	15	123.5	5.3	1010	11	Q7TQ89	Q7tq89 rattus norv
	16	123	5.3	508	13	Q9YHV9	Q9yvh9 gallus gall
30	17	122	5.2	1734	11	Q9JIQ9	Q9jiq9 rattus norv
	18	121	5.2	442	13	Q9PVJ9	Q9pvj9 gallus gall
	19	120	5.2	229	11	Q7TNI4	Q7tni4 rattus norv
	20	120	5.2	2187	4	Q9H197	Q9h197 homo sapien
35	21	120	5.2	2254	4	Q9HCY0	Q9hcy0 homo sapien
	22	118	5.1	569	13	Q9YHW0	Q9yhw0 gallus gall
	23	117.5	5.1	707	11	Q8BW61	Q8bw61 mus musculu
	24	116.5	5.0	1156	16	Q8F2J8	Q8f2j8 leptospira
40	25	116	5.0	354	5	O62430	O62430 caenorhabdi
	26	116	5.0	574	4	Q8N6P7	Q8n6p7 homo sapien
	27	116	5.0	655	16	Q7UQU2	Q7uqu2 rhodopirell
	28	116	5.0	1893	11	Q8CJ14	Q8cj14 rattus norv
45	29	115	4.9	896	11	Q8QZX9	Q8qzx9 mus musculu
	30	115	4.9	965	4	Q7Z344	Q7z344 homo sapien
	31	115	4.9	2957	5	O61845	O61845 caenorhabdi
	32	115	4.9	3198	5	Q9U8G8	Q9u8g8 manduca sex
50	33	114.5	4.9	737	11	Q8BW83	Q8bw83 mus musculu
	34	114.5	4.9	1023	2	Q93T53	Q93t53 streptococc
	35	114	4.9	574	4	Q9HB22	Q9hb22 homo sapien
	36	113	4.9	672	16	Q8UA29	Q8ua29 agrobacteri
55	37	113	4.9	2297	3	Q9HGK6	Q9hkg6 candida alb
	38	112	4.8	231	4	Q96A41	Q96a41 homo sapien
	39	112	4.8	263	4	Q969J5	Q969j5 homo sapien
	40	112	4.8	382	16	Q99YV5	Q99yv5 streptococc
55	41	112	4.8	382	16	Q8K6R8	Q8k6r8 streptococc
	42	112	4.8	1089	5	O44007	O44007 dictyosteli
	43	111	4.8	338	13	Q800G2	Q800g2 tetraodon n
	44	111	4.8	382	16	Q8P064	Q8p064 streptococc
	45	111	4.8	443	6	Q7YQN5	Q7yqn5 megaderma 1